

GenCore version 5.1.6  
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### On protein - protein search, using sw model

Run on: November 3, 2005, 21:37:29 ; Search time 91.4866 Seconds

291.060 Million cell updates/sec

Title: 09782816-51

Perfect score: 251

Sequence: 1 GYKETPOCKYQRLHLHEVQEL.....ESATEBKLTIVLAKQLAL 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03;\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	251	100.0	400	1	DCT2_HUMAN
2	248	98.8	401	1	DCT2_MOUSE
3	248	98.8	402	2	Q6LYH5
4	220	87.6	403	2	Q6LRB3
5	213	84.9	403	2	Q6WJ30
6	211	84.1	2	Q7ZXY2	
7	177	70.5	402	2	Q8PTG6
8	177	70.5	405	2	Q7T3H1
9	76	30.3	402	2	Q8TP53
10	72.5	28.9	380	2	Q914Y9
11	71	28.3	800	2	Q5WV7
12	71	28.3	813	2	Q7SH14
13	70	27.9	311	2	Q9T1V5
14	70	27.9	751	2	Q8NQK1
15	70	27.9	1087	2	Q8B8S5
16	70	27.9	1124	2	Q8BQJ8
17	70	27.9	2199	2	Q7PUP2
18	69.5	27.7	873	2	Q95X55
19	69.5	27.7	919	2	Q95X55
20	68	27.1	1755	2	Q7RV31
21	68	27.1	1968	2	Q8XOC5
22	67.5	26.9	1868	2	Q8BNV2
23	67	26.7	455	2	Q7ZVF1
24	67	26.7	639	2	Q6Z245
25	67	26.7	1795	2	Q91CJ9
26	67	26.7	2478	2	Q91CH2
27	67	26.7	2478	2	Q8R69
28	67	26.7	2481	2	Q99QR6
29	67	26.7	2481	2	Q7A4B1
30	66	26.3	393	2	Q49567
31	66	26.3	860	2	Q7Q0Q9

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Listing first 45 summaries

Database : UniProt\_03;\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

### ALIGNMENTS

RESULT 1

DCT2\_HUMAN STANDARD; PRT; 400 AA.

ID DCT2\_HUMAN

AC Q13561; Q86YN2; Q9BW17;

DT 01-NOV-1997 (Rel. 35, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DR Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide)

DB (p50 dyminatin) (DCTN-50) (Dynactin 2).

GN Name=DCTN2; Synonyms=DCTN50;

OS Homo sapiens (Human).

OC Burkartyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo;

OX NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE

RX MEDLINE-96178092, PubMed-8647983, DOI=10.1083/jcb.132.4.617;

RX Bacheverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;

RT "Molecular characterization of the 50-kb subunit of dyneactin reveals

RT function for the complex in chromosome alignment and spindle

RT organization during mitosis";

J. Cell Biol. 132:617-633(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta, Skin, and Uterus;

RX MEDLINE=22388257; PubMed=1427932; DOI=10.1073/pnas.242603899;

RX Stranberg R.L., Feingold E.A., Grouse L.H., Derge J.G..

RX Klauner R.D., Collins F.S., Wagner L., Sheeney C.M., Schuler G.D.,

RX Altshul S.F., Zeeberg B., Bustow K.H., Schefer C.F., Bhat N.K.,

RX Hopkins R.F., Jordahn H., Moore T., Max S.I., Wang J., Heile F.,

RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Stapleton M., Soates M.B., Bonaldo M., Casavant T.L., Scheetz T.E.,

RX Brownstein M.J., Usdin T.B., Toshimuki S., Carninci P., Prange C.,

RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guanarate R.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,

RX Villon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RX Pahey J., Helton B., Ketteam M., Madan A., Rodriguez S., Sanchez A.,

RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RX Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.B.,

RX Schnarch A., Schein J.B., Jones S.J.M., Marra M.A., submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

084500 chlamydia t  
08tb8 homo sapien  
074424 schizosacch  
07pz25 anopheles g  
081i9 orya sativ  
09bz3 homo sapien  
09um0 homo sapien  
092113 mus musculus  
06dg9 brachydiplo  
09bi3 arachidopis  
075545 homo sapien  
09gf1 draconophila  
09y2k3 homo sapien  
P51714 bacteriopha

Exhibit 4  
20 F2

RC TISSUE=Plateslet;  
 RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;  
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,  
 RA Thomas G.R., Vandekerckhove J.;  
 RT "Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides";  
 RL Nat. Biotechnol. 21:566-569(2003).  
 -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spindle organization during mitosis. May play a role in synapse formation during brain development.  
 -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated with dynein.  
 -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.

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CC EMBL; US0733; AAC50423.1; -.  
 DR EMBL; BC000718; AAC00718.1; -.  
 DR EMBL; BC009468; AAC09468.1; -.  
 DR EMBL; BC014083; AAC014083.1; -.  
 DR EMBL; AY189155; AA034395.1; -.  
 DR Genew; HGNC:2712; DCTN2.  
 DR MIM; 607376; -.  
 DR GO; GO:0005813; C:centrosome; TAS.  
 DR GO; GO:0005659; C:dynein complex; TAS.  
 DR GO; GO:0007776; C:kintechore; TAS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR GO; GO:0007067; P:mitosis; TAS.  
 DR Interpro; IPR006996; Dynamin.  
 DR Pfam; PF04912; Dynamin; 1.  
 KW Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 KW Membrane; Microtubule; Motor protein.  
 PT INIT\_MET 0  
 PT DOMAIN 98 131 Coiled coil (Potential).  
 PT DOMAIN 213 243 Coiled coil (Potential).  
 PT DOMAIN 378 398 Coiled coil (Potential).  
 PT DOMAIN 34 34 A > APAQEL (in Ref. 1).  
 PT CONFLICT 35 35 B > ELE (in Ref. 3).  
 PT CONFLICT 381 384 LATV > PRHS (in Ref. 3).  
 PT SEQUENCER 400 AA; 44099 MW; QAS5AB95C0BB270P CRC64;

Query Match Best Local Similarity 100.0%; Score 251; DB 1; Length 400; Matches 52; Conservative 0; Mismatches 0; Gaps 0;

Oy 1 GVKETPOQKQYRQLLHEVOELTEVERKTTWESATEBKUTPVLLAKQAL 52  
 Db 93 GVKETPOQKQYRQLLHEVOELTEVERKTTWESATEBKUTPVLLAKQAL 144

RESULT 2

DCT2\_MOUSE ID\_DCT2\_MOUSE STANDARD; PRT; 401 AA.  
 AC 099KU8;  
 DT 28-Feb-2003 (Rel. 41, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DB Dynactin complex 50 kDa subunit (50 kDa dynein-associated polypeptide) (50 dyanitin) (DCTN-50) (Dynactin 2) (Growth cone membrane protein (23-48k) (GMP23-48k)).  
 GN Name=DCTN2;  
 SN *musculus* (Mouse);  
 SA *lakaryota*; *Metazoa*; *Chordata*; *Craniata*; *Vertebrata*; *Euteleostomi*; *Mammalia*; *Butheria*; *Rodentia*; *Sciurognathi*; *Muridae*; *Murinae*; *Mus*.  
 NSI TAXID=10090;

RP SEQUENCE FROM N-A.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.D., Reingold E.A., Grouse L.H., Degege J.G.,  
 RA Klauner R.D., Collins P.S., Wagner L., Shearer C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Udin N.T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lourenco N.A., Peters G.J., Abramson R.D., Mullahay S.J.,  
 RA Bosak S.A., McEwan P.J., McFernan K.J., Malek J.A., Gunnarino P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska O., Smialius D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.,";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903 (2002).  
 RN [2]  
 RP SEQUENCE OF 65-74; 77-91; 102-116; 156-170; 194-216 AND 309-320,  
 RP SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RN [3]  
 RP INTERACTION WITH BICD2.  
 RX MEDLINE=2137652; PubMed=11483508; DOI=10.1093/embj/20.15.4041;  
 RA Hoogenraad C.C., Alchmanova A., Howell S.A., Dorland B.R.,  
 RA de Zeeuw C.I., Willmesen R., Visser P., Grosveld F., Galjart N.;  
 RT "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-  
 RT dynein pathway by interacting with these complexes.,";  
 RL EMBO J. 20:401-4054 (2001).  
 CC -!- FUNCTION: Modulates cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spindle organization during mitosis. May play a role in synapse formation during brain development.  
 CC -!- SUBUNIT: Subunit of dynein, a multiprotein complex associated with dynein (BY similarity). Interacts with BICD2.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC -!- DEVELOPMENTAL\_STAGE: Present at high levels in both cytoplasmic and membrane-associated forms in rodonates. Levels of membrane-associated form are greatly reduced in the adult.

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CC EMBL; BC004613; AA04613.1; -.  
 DR MGD; MG1:10773; Dctn2.  
 DR InterPro; IPR06996; Dynamin; 1.  
 PT Pfam; PF04912; Dynamin; 1.  
 PT Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;  
 PT Membrane; Microtubule; Motor protein.  
 PT INIT\_MET 0  
 PT DOMAIN 98 131 Coiled coil (Potential).  
 PT DOMAIN 214 244 Coiled coil (Potential).  
 PT SEQUENCE 401 AA; 43985 MW; 1535B4ABD5940BBC CRC64;

Query Match Best Local Similarity 98.8%; Score 248; DB 1; Length 401; Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;